


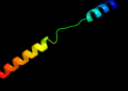








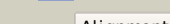

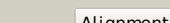







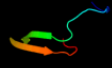
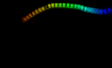
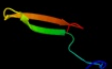



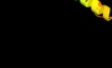




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2uval_	 Alignment		49.7	17	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
2	c3t97B_	 Alignment		46.2	21	PDB header: protein transport Chain: B: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54
3	c2gl2B_	 Alignment		40.5	14	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
4	c1jccC_	 Alignment		36.4	23	PDB header: membrane protein Chain: C: PDB Molecule: major outer membrane lipoprotein; PDBTitle: crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,l16a,v20a,l23a,v27a,m30a,v34a mutations
5	c3pubA_	 Alignment		32.9	33	PDB header: unknown function Chain: A: PDB Molecule: 30kda protein; PDBTitle: crystal structure of the bombyx mori low molecular weight lipoprotein2 7 (bm1p7)
6	d1wu9a1	 Alignment		26.1	27	Fold: EB1 dimerisation domain-like Superfamily: EB1 dimerisation domain-like Family: EB1 dimerisation domain-like
7	c2w0cR_	 Alignment		24.5	37	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing2 bacteriophage pm2
8	c1ce0B_	 Alignment		22.8	32	PDB header: hiv-1 envelope protein Chain: B: PDB Molecule: protein (leucine zipper model h38-p1); PDBTitle: trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
9	c3ocaB_	 Alignment		19.2	23	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of peptide deformylase from ehrlichia chaffeensis
10	d1g3wa2	 Alignment		17.0	8	Fold: Iron-dependent repressor protein, dimerization domain Superfamily: Iron-dependent repressor protein, dimerization domain Family: Iron-dependent repressor protein, dimerization domain
11	d2d0ta1	 Alignment		16.0	16	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like

12	c3qu1B_	Alignment		15.1	11	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: peptide deformylase 2; PDBTitle: peptide deformylase from vibrio cholerae
13	c1ei3E_	Alignment		14.0	11	PDB header: PDB COMPND:
14	c1ws1A_	Alignment		13.4	23	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase 1; PDBTitle: structure analysis of peptide deformylase from bacillus2 cereus
15	c1gk6B_	Alignment		13.0	20	PDB header: vimentin Chain: B: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
16	d1u84a_	Alignment		12.9	8	Fold: YugE-like Superfamily: YugE-like Family: YugE-like
17	c3qmzA_	Alignment		12.6	14	PDB header: motor protein Chain: A: PDB Molecule: cytoplasmic dynein heavy chain; PDBTitle: crystal structure of the cytoplasmic dynein heavy chain motor domain
18	c2pmzL_	Alignment		12.5	12	PDB header: translation, transferase Chain: L: PDB Molecule: dna-directed rna polymerase subunit I; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
19	d1txqb1	Alignment		12.4	29	Fold: EB1 dimerisation domain-like Superfamily: EB1 dimerisation domain-like Family: EB1 dimerisation domain-like
20	c1txqB_	Alignment		12.4	29	PDB header: structural protein/protein binding Chain: B: PDB Molecule: microtubule-associated protein rp/eb family PDBTitle: crystal structure of the eb1 c-terminal domain complexed2 with the cap-gly domain of p150glued
21	c1u0iA_	Alignment	not modelled	12.3	55	PDB header: de novo protein Chain: A: PDB Molecule: iaal-e3; PDBTitle: iaal-e3/k3 heterodimer
22	c3movB_	Alignment	not modelled	11.6	11	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of human lamin-b1 coil 2 segment
23	c1gcmA_	Alignment	not modelled	11.3	25	PDB header: transcription regulation Chain: A: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
24	c3ag7A_	Alignment	not modelled	11.3	22	PDB header: plant protein Chain: A: PDB Molecule: putative uncharacterized protein f9e10.5; PDBTitle: an auxilin-like j-domain containing protein, jac1 j-domain
25	c3u1aC_	Alignment	not modelled	11.2	22	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
26	c3ca9A_	Alignment	not modelled	11.2	18	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
27	c2cpbA_	Alignment	not modelled	11.0	57	PDB header: viral protein Chain: A: PDB Molecule: m13 major coat protein; PDBTitle: solution nmr structures of the major coat protein of2 filamentous bacteriophage m13 solubilized in3 dodecylphosphocholine micelles, 25 lowest energy structures
28	c1x8yA_	Alignment	not modelled	10.4	13	PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b
						PDB header: hydrolase

29	c2ew7A_	Alignment	not modelled	10.1	6	Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of helicobacter pylori peptide deformylase
30	c1gcmC_	Alignment	not modelled	9.8	25	PDB header: transcription regulation Chain: C: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
31	c1ox3A_	Alignment	not modelled	9.7	15	PDB header: chaperone Chain: A: PDB Molecule: fibritin; PDBTitle: crystal structure of mini-fibritin
32	c1gk4A_	Alignment	not modelled	9.6	13	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)
33	c2xv5A_	Alignment	not modelled	9.5	13	PDB header: structural protein Chain: A: PDB Molecule: lamin-a/c; PDBTitle: human lamin a coil 2b fragment
34	c3g5pB_	Alignment	not modelled	9.3	23	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase, mitochondrial; PDBTitle: structure and activity of human mitochondrial peptide deformylase, a2 novel cancer target
35	c1ij1B_	Alignment	not modelled	9.1	36	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
36	c1ij1C_	Alignment	not modelled	9.1	36	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
37	c1ij1A_	Alignment	not modelled	9.1	36	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
38	d1lmea_	Alignment	not modelled	9.0	20	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
39	d1lm4a_	Alignment	not modelled	9.0	20	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
40	c1gcmB_	Alignment	not modelled	9.0	23	PDB header: transcription regulation Chain: B: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
41	dlix1a_	Alignment	not modelled	8.9	26	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
42	d1ujka_	Alignment	not modelled	8.7	9	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
43	d1zuea1	Alignment	not modelled	8.7	31	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
44	c1ij0A_	Alignment	not modelled	8.7	36	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: coiled coil trimer gcn4-pvls ser at buried d position
45	c1ij0B_	Alignment	not modelled	8.7	36	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: coiled coil trimer gcn4-pvls ser at buried d position
46	c1ij0C_	Alignment	not modelled	8.7	36	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: coiled coil trimer gcn4-pvls ser at buried d position
47	d1v54e_	Alignment	not modelled	8.4	25	Fold: alpha-alpha superhelix Superfamily: Cytochrome c oxidase subunit E Family: Cytochrome c oxidase subunit E
48	d2defa_	Alignment	not modelled	8.3	17	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
49	d1y6ha_	Alignment	not modelled	8.2	20	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
50	c3g6nA_	Alignment	not modelled	8.0	18	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of an efpdf complex with met-ala-ser
51	d3saka_	Alignment	not modelled	7.9	17	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
52	c2y9zA_	Alignment	not modelled	7.8	17	PDB header: transcription Chain: A: PDB Molecule: imitation switch protein 1 (del_atpase); PDBTitle: chromatin remodeling factor isw1a(del_atpase) in dna complex
53	c2w3tA_	Alignment	not modelled	7.5	17	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: chloro complex of the ni-form of e.coli deformylase
54	c2ko6A_	Alignment	not modelled	7.3	64	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yihd; PDBTitle: solution structure of protein sf3929 from shigella flexneri2 2a. northeast structural genomics consortium target3 sfr81/ontario center for structural proteomics target4 sf3929
55	c1zy1B_	Alignment	not modelled	7.1	11	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase, mitochondrial; PDBTitle: x-ray structure of peptide deformylase from arabidopsis2 thaliana (atpdf1a) in complex with met-ala-ser

56	c1deqF_	Alignment	not modelled	6.9	12	PDB header: PDB COMPND:
57	d2gu3a2	Alignment	not modelled	6.9	19	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: PepSY-like
58	c1gcIB_	Alignment	not modelled	6.8	25	PDB header: leucine zipper Chain: B: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
59	c1gcIA_	Alignment	not modelled	6.8	25	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
60	c1gcIC_	Alignment	not modelled	6.8	25	PDB header: leucine zipper Chain: C: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
61	c1gcID_	Alignment	not modelled	6.8	25	PDB header: leucine zipper Chain: D: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
62	c3g9rF_	Alignment	not modelled	6.7	33	PDB header: viral protein Chain: F: PDB Molecule: fusion complex of hiv-1 envelope glycoprotein PDBTitle: structure of the hiv-1 gp41 membrane-proximal ectodomain2 region in a putative prefusion conformation
63	c3ecyA_	Alignment	not modelled	6.7	11	PDB header: hydrolase Chain: A: PDB Molecule: cg4584-pa, isoform a (bcdna.l08534); PDBTitle: crystal structural analysis of drosophila melanogaster dutpase
64	c3ahrA_	Alignment	not modelled	6.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
65	c1ic2B_	Alignment	not modelled	6.7	26	PDB header: contractile protein Chain: B: PDB Molecule: tropomyosin alpha chain, skeletal muscle; PDBTitle: deciphering the design of the tropomyosin molecule
66	c3f3hA_	Alignment	not modelled	6.6	33	PDB header: antitumor protein Chain: A: PDB Molecule: immunomodulatory protein ling zhi-8; PDBTitle: crystal structure and anti-tumor activity of lz-8 from the fungus2 ganoderma lucidium
67	c2pjwV_	Alignment	not modelled	6.5	7	PDB header: endocytosis/exocytosis Chain: V: PDB Molecule: vacuolar protein sorting-associated protein 27; PDBTitle: the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
68	c3dlIdA_	Alignment	not modelled	6.3	17	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of peptide deformylase, xoo1075, from2 xanthomonas oryzae pv. oryzae kacc10331
69	c1ij2C_	Alignment	not modelled	6.3	36	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
70	c1unxA_	Alignment	not modelled	6.3	25	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
71	c1rb1B_	Alignment	not modelled	6.2	36	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
72	c1rb1A_	Alignment	not modelled	6.2	36	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
73	c1swiA_	Alignment	not modelled	6.2	36	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4p1; PDBTitle: gcn4-leucine zipper core mutant as n16a complexed with2 benzene
74	c3k7zB_	Alignment	not modelled	6.2	36	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
75	c1rb6C_	Alignment	not modelled	6.2	36	PDB header: dna binding protein Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
76	c3k7zA_	Alignment	not modelled	6.2	36	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
77	c3ieeA_	Alignment	not modelled	6.2	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of hypothetical protein bf3319 from bacteroides2 fragilis (yp_212931.1) from bacteroides fragilis nctc 9343 at 1.70 a3 resolution
78	c1uo2A_	Alignment	not modelled	6.1	25	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
79	c1w5iA_	Alignment	not modelled	6.1	25	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: aba does not affect topology of pli.
80	c3lvwA_	Alignment	not modelled	6.0	30	PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase; PDBTitle: glutathione-inhibited scgcl
81	c1unwB_	Alignment	not modelled	6.0	25	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles

82	c1ij3C_	Alignment	not modelled	6.0	36	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
83	c1ij3B_	Alignment	not modelled	6.0	36	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
84	c3hizB_	Alignment	not modelled	5.9	15	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit PDBTitle: crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
85	c3cpmA_	Alignment	not modelled	5.9	14	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase, chloroplast; PDBTitle: plant peptide deformylase pdf1b crystal structure
86	c1uo1A_	Alignment	not modelled	5.9	25	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
87	c1uo1B_	Alignment	not modelled	5.9	25	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
88	d1xeoa1	Alignment	not modelled	5.9	17	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
89	c1ij2A_	Alignment	not modelled	5.9	36	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
90	c1w5iB_	Alignment	not modelled	5.8	25	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: aba does not affect topology of pli.
91	c1uo2B_	Alignment	not modelled	5.8	25	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
92	c1uo0A_	Alignment	not modelled	5.8	25	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
93	c1uo0B_	Alignment	not modelled	5.8	25	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
94	c1rb4C_	Alignment	not modelled	5.7	36	PDB header: dna binding protein Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution
95	c3lp6D_	Alignment	not modelled	5.7	10	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
96	d1rl4a_	Alignment	not modelled	5.7	14	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
97	d2axto1	Alignment	not modelled	5.6	29	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: PsbO-like
98	c1ij2B_	Alignment	not modelled	5.6	36	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
99	c1rb4A_	Alignment	not modelled	5.5	36	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution